

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 10:52:07 ; Search time 2658.23 Seconds

(without alignments)
4226.338 Million cell updates/sec

Title: US-09-602-833a-3

Perfect score: 681

Sequence: 1 atcagaattcgtgatcgc.....ctttagcctcaatttga 681

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_ov:*

21: em_or:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

8

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	681	100.0	681	6	AX063234	AX063234 Sequence
2	681	100.0	1116	6	AX063232	AX063232 Sequence
3	681	100.0	4860	9	HSA308569	AJ308569 Homo sapi
4	392.8	57.7	172966	9	AC013467	AC013467 Homo sapi
5	161	23.6	145795	2	HSN310996	AJ310996 Homo sapi
6	161	23.6	202324	2	AC068720	AC068720 Homo sapi
7	137.8	20.2	202324	2	AC068720	AC068720 Homo sapi
8	130.4	19.1	2056	9	AK021919	AK021919 Homo sapi
9	60.8	8.9	1658	9	AF359380	AF359380 Homo sapi
10	60.8	8.9	2156	9	BC003193	BC003193 Homo sapi
11	59.8	8.9	2886	9	AF332199	AF332199 Homo sapi
12	59.8	8.8	216481	2	AC027653	AC027653 Mus muscu
13	58.2	8.5	133841	2	AC079990	AC079990 Rattus no
14	58.2	8.5	168150	2	AC079378	AC079378 Rattus no
15	57.4	8.4	1127	9	AY007147	AY007147 Homo sapi
16	57.4	8.4	2384	6	AX099399	AX099399 Sequence
17	57.4	8.4	162598	2	AC079091	AC079091 Homo sapi
18	57.4	8.4	174297	2	AL512367	AL512367 Homo sapi
19	57.4	8.4	212127	2	AL391497	AL391497 Homo sapi
20	56.8	8.3	182366	2	AC041041	AC041041 Homo sapi
21	56.8	8.3	182885	2	AC087763	AC087763 Homo sapi
22	56.8	8.3	182914	2	AC090567	AC090567 Homo sapi
23	56.8	8.3	185510	2	AC011018	AC011018 Homo sapi
24	55.8	8.2	2410	9	AK001332	AK001332 Homo sapi
25	55.2	8.1	3159	9	AB016816	AB016816 Homo sapi
26	55.2	8.1	6125	6	AX188327	AX188327 Sequence
27	54.4	8.0	142296	2	AF004035	AF004035 Homo sapi
28	54.4	8.0	142396	2	HSAC000120	AC000120 Human BAC
29	54.4	8.0	169580	2	AC092762	AC092762 Pan trogl
30	54.4	8.0	257967	2	AL365337	AL365337 Mus muscu
31	52.8	7.8	4635	3	DME271647	AJ271647 Drosophill
32	52.8	7.8	5988	3	AF190774	AF190774 Drosophill
33	52.8	7.8	7166	3	DME232084	AJ232084 Drosophill
34	52.6	7.7	2893	3	BC009239	BC009239 Homo sapi
35	52.6	7.7	118533	2	AC020205	AC020205 Drosophill
36	52.6	7.7	165852	2	AC092874	AC092874 Sus scrofa
37	52.6	7.7	173970	3	AC005286	AC005286 Drosophill
38	52.6	7.7	263693	3	AE003793	AE003793 Drosophill
39	51.4	7.5	8373	8	AF290191	AF290191 Cryptococ
40	51.2	7.5	156294	2	AC092409	AC092409 Papio cyn
41	51.2	7.5	198746	2	AC092517	AC092517 Papio cyn
42	51	7.5	6248	9	D86984	D86984 Human mRNA
43	50.4	7.4	2620	9	AK001637	AK001637 Homo sapi
44	50.4	7.4	2754	9	BC003407	BC003407 Homo sapi
45	50.4	7.4	2846	9	BC008586	BC008586 Homo sapi

ALIGNMENTS

RESULT	1	AX063234	681 bp	DNA	PAT	24-JAN-2001
LOCUS	AX063234					
DEFINITION	Sequence 3 from Patent WO0070959.					
ACCESSION	AX063234					
VERSION	AX063234.1		GI:12541060			
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiiniidae; Homo.					
AUTHORS	Turner,A.C., Zambrowicz,B., Nehls,M., Friedrich,G.A. and Sands,A.T.					
TITLE	Human genes and proteins encoded thereby					
JOURNAL	Patent: WO 0078959-A 3 28-DEC-2000;					
FEATURES	Lexicon Genetics Incorporated (US)					
source	Location/Qualifiers					
	1..681					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					

QY 601 aaagcctatattgagacctaagaagaatcgttccagctataccaccaagtg 660
|||||
Db 1036 AAAGCCTATATTGAAGACCTTAAGAAAGAAATCTGTCCAGCTATACCAACCAAGTG 1095
QY 661 tcttttagcctccaacttga 681
|||||
Db 1096 TCTTTAGCCTTCAACTTTGA 1116
|||||
RESULT 3
HSA308569 4860 bp mRNA PRI 06-JUN-2001
LOCUS Homo sapiens mRNA for leucine-rich repeat-containing 2 protein
DEFINITION (LRRC2 gene).
ACCESSION AJ308569
VERSION AJ308569.2 GI:14330408
KEYWORDS leucine-rich repeat-containing 2 protein; LRRC2 gene.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4860)
AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I.,
Kedra, D., Kiss, C., Klein, G., Imreh, S. and Dunamski, J. P.
TITLE Transcriptional map of the Common Eliminated Region 1 on human
3p21.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4860)
AUTHORS Kiss, H.
JOURNAL Direct Submission
Submitted (27-FEB-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
REMARK Revised by [3]
REFERENCE 3 (bases 1 to 4860)
AUTHORS Kiss, H.
JOURNAL Direct Submission
Submitted (06-JUN-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT On Jun 8, 2001 this sequence version replaced gi:13186111.
FEATURES
source
Location/Qualifiers
1..4860
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.3"
168..1283
/gene="LRRC2"
168..1283
/gene="LRRC2"
/codon_start=1
/product="leucine-rich repeat-containing 2 protein"
/protein_id="CAC33442.1"
/db_xref="GI:13186112"
/translation="MGHKVVPDVISVIALMETRVKKHKKMOKKEVERLEKSALEKIK
EENVPFAECRRKGIPOAVYCKNGFIDTSVGLTKIRNLTROSSIPKDKRSSAFV
FELSGHMELEPDSLIKQOTLRMYISNTLIQIIPYIQIFQMRITLDPKNOISHP
AETGCKLNKLELVGNFYRLKSTIPEDLDCENLRDSCGNLELMELEPFLSNLKQYTF
VDTSANKLFSSVPIVCVSRMSNLQWLDISSNNLTLPDIDIDLELQSLVLYKNLTLP
YSMLNKLKTLVLVSGDHLVLEPTALDCDSSTPLKFSVLSIMNPIDNACEDGNEIMSE
RDRQHFDEVMKAYIEDIKERESVPSYTTKVSFSLQ"
BASE COUNT 1480 a 924 c 1162 g 1294 t
ORIGIN
Query Match 100.0%; Score 681; DB 9; Length 4860;
Best Local Similarity 100.0%; Pred. No. 4.8e-168;
Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggaattcgtgactcgtgcaaaaacaaatccacacattccagcagaatcgtgtg 60
|||||

Db 603 ATGGAATTCCTGACTCTGCCAAAAACCAAAATCTACATCTTCCAGCAGAAATGCTTGT 662
QY 61 ttgaagaacctgaagaactcaatggtttcaactatctgaagacattcccgaa 120
|||||
Db 663 TTGAAGACCTGAANAAGCTCAATGTGGGTTCACTATCTGAAGAGATTCTCCAGAA 722
QY 121 ttggagatttgaaaaactagagagactgattgtctctggaactcagaattaatgag 180
723 TTGGAGATTGTGAANAATCTAGAGAGACTGATGTGTTCTGSAATCTAGATTTATGAG 782
QY 181 ctgcctttgaattaagaatttgaagaagttacattttagatlatccagaacaag 240
Db 783 CTGCCCTTTGAATTAAGTAATTTGAGCAAGTTACATTTTGAGATATCTCAGAAACAG 842
QY 241 ttccacagtcaccaactcgtcgtctcgagatgcgaatttgcagtggttgatatagc 300
Db 843 TTTTCAGTGTCCCAATCTGTCTCGGATGTCGAATTTGCAGTGGTGGATATACG 902
QY 301 agcaataacctgaccgacctcgcaagatatagacagctagaaggagctcagaagctt 360
Db 903 AGCAATAACCTGACCGACCTGCCGCAAGATATAGACAGCTAGAGAGCTCAGAGCTTT 962
QY 361 ctcttgataaacaagttgacctaccctccattccatcaltgctgaacctgaagaagctc 420
Db 963 CTTTGTGATATAAACAAGTTGACCTACCTTCCATTCCATGCTGAACCTGAAGAGCTC 1022
QY 421 actctgttagtcgctcagtgaggaccatttggtagagctcccaactgccttggactca 480
Db 1023 ACTCTGTAGTCGTCAGGGGAGACCTTTGGTGAAGCTCCCACTGCCCTTTGATCTCA 1082
QY 481 tccacaccttaaaatctgtaagcctatagacaatccatattgataatgccaatgtaa 540
Db 1083 TCCACACCTTAAATTTGTAGGCTTATGACATCTATTTGATATGCCCATGTGAA 1142
QY 541 gatggcaatgaataatgagaagtgaacggagatcgccacaacatttgataaagaagtatg 600
Db 1143 GATGGCAATGAATAATGAGAAATGAAACGGGATGCCCAACATTTGATTAAGAAGTATG 1202
QY 601 aaagcctatattgagacctaagaagaagaatcttccagctataccaccaagtg 660
Db 1203 AAAGCCTATATTGAAGACCTTAAGAAAGAAATCTGTCCAGCTATACCAACCAAGTG 1262
QY 661 tcttttagcctccaacttga 681
Db 1263 TCTTTAGCCTTCAACTTTGA 1283
|||||
RESULT 4
AC013467/c 172966 bp DNA PRI 25-MAY-2001
LOCUS Homo sapiens clone RP11-451F14, complete sequence.
DEFINITION AC013467
ACCESSION AC013467.8 GI:14196420
VERSION HTG.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 172966)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 172966)
AUTHORS Waterston, R. H.
JOURNAL Direct Submission
Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 172966)
AUTHORS Waterston, R. H.
JOURNAL Direct Submission
Submitted (25-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,


```

* 75556 75655: gap of 100 bp
* 75656 77760: contig of 2105 bp in length
* 77761 77860: gap of 100 bp
* 77861 79686: contig of 1826 bp in length
* 79687 79786: gap of 100 bp
* 79787 80857: contig of 1071 bp in length
* 80858 80957: gap of 100 bp
* 80958 87622: contig of 6665 bp in length
* 87623 87722: gap of 100 bp
* 87723 89164: contig of 1442 bp in length
* 89165 89264: gap of 100 bp
* 89265 90007: contig of 743 bp in length
* 90008 90107: gap of 100 bp
* 90108 92035: contig of 1928 bp in length
* 92036 92135: gap of 100 bp
* 92136 97298: contig of 5163 bp in length
* 97299 97398: gap of 100 bp
* 97399 102032: contig of 4634 bp in length
* 102033 102132: gap of 100 bp
* 102133 106605: contig of 4473 bp in length
* 106606 106705: gap of 100 bp
* 106706 108263: contig of 1558 bp in length
* 108264 108363: gap of 100 bp
* 108364 110022: contig of 1659 bp in length
* 110023 110122: gap of 100 bp
* 110123 113747: contig of 3625 bp in length
* 113748 113847: gap of 100 bp
* 113848 125151: contig of 11304 bp in length
* 125152 125251: gap of 100 bp
* 125252 126026: contig of 775 bp in length
* 126027 126126: gap of 100 bp
* 126127 129649: contig of 3523 bp in length
* 129650 129749: gap of 100 bp
* 129750 132160: contig of 2411 bp in length
* 132161 132260: gap of 100 bp
* 132261 133125: contig of 865 bp in length
* 133126 133225: gap of 100 bp
* 133226 135661: contig of 2436 bp in length
* 135662 135761: gap of 100 bp
* 135762 142148: contig of 6387 bp in length
* 142149 142248: gap of 100 bp
* 142249 145795: contig of 3547 bp in length.

FEATURES
    source
        1. 145795
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="3"
            /map="3p21.3"
            /clone="RP6-91P17"

BASE COUNT    39764 a 33207 c 31499 g 37225 t 4100 others
ORIGIN
Query Match    23.6%; Score 161, DB 2; Length 145795;
Best Local Similarity 97.0%; Pred. No. 2e-31;
Matches 164; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 337 agcctagaagcgtgcgcagccttctctgtatataaacaagtgtacctctccctat 396
Db 61617 AGCCTAAGAGAGCTGCAGACCTTCTGTGATPAAAAACAAGTGTGACCTTCCCTAT 61558

QY 397 tccatgctgaacctgaagaagctcaactctgtatagctcagtgaggacattgtgag 456
Db 61557 TCCATGCTGAACCTGAAGAAGCTCACTGTGATTAAGTGTGAGGACCATTTGTGAG 61498

QY 457 ctcccaactgcaccttctgtgaactcaccacaccttaaatgtgaagc 505
Db 61497 CTCCTCACTGCCCTTTGTGACTCATCCACACCTTTAAGTGATGAGCCC 61449

RESULT 6
AC068720 AC068720 202324 bp DNA HTG 07-JUL-2000

```

```

DEFINITION Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
SEQUENCE 20 unordered pieces.
AC068720
VERSION AC068720.2 GI:8469022
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 202324)
REFERENCE Waterston,R.H.
AUTHORS The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202324)
AUTHORS Waterston,R.H.
TITLE Direct Submission
SUBMITTED (07-MAY-2000) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 12, 2000 this sequence version replaced gi:7715661.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0509121
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 195686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-fp
Quality coverage: 4.67 in Q20 bases; agarose-fp
Quality coverage: 4.72 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
-----
1 1576: contig of 1576 bp in length
* 1577 1676: gap of unknown length
* 1677 3263: contig of 1587 bp in length
* 3264 3363: gap of unknown length
* 3364 5443: contig of 2080 bp in length
* 5444 5543: gap of unknown length
* 5544 8196: contig of 2653 bp in length
* 8197 8296: gap of unknown length
* 8297 12038: contig of 3742 bp in length
* 12039 12138: gap of unknown length
* 12139 15992: contig of 3854 bp in length
* 15993 16092: gap of unknown length
* 16093 21192: contig of 5100 bp in length
* 21193 21292: gap of unknown length
* 21293 24766: contig of 3474 bp in length
* 24767 24866: gap of unknown length
* 24867 30824: contig of 5958 bp in length
* 30825 30924: gap of unknown length
* 30925 37154: contig of 6229 bp in length
* 37154 37253: gap of unknown length
* 37254 45262: contig of 8009 bp in length
* 45263 45362: gap of unknown length
* 45363 56733: contig of 11371 bp in length
* 56734 56833: gap of unknown length

```


*	8297	12038	contig of 3742 bp in length
*	12039	15992	contig of unknown length
*	12139	15992	contig of 3854 bp in length
*	15993	16092	gap of unknown length
*	16093	21192	contig of 5100 bp in length
*	21193	21292	gap of unknown length
*	21293	24766	contig of 3474 bp in length
*	24767	24866	gap of unknown length
*	24867	30824	contig of 5958 bp in length
*	30825	30924	gap of unknown length
*	30925	37153	contig of 6229 bp in length
*	37154	37253	gap of unknown length
*	37254	45262	contig of 8009 bp in length
*	45263	45363	gap of unknown length
*	45363	56833	contig of 11371 bp in length
*	56734	56833	gap of unknown length
*	56834	72135	contig of 15323 bp in length
*	72135	72256	gap of unknown length
*	72157	84702	contig of 12446 bp in length
*	72257	84702	gap of unknown length
*	84703	84802	contig of 16250 bp in length
*	84803	101053	gap of unknown length
*	101053	101152	gap of unknown length
*	101153	117709	contig of 16537 bp in length
*	117710	117809	gap of unknown length
*	117810	132550	contig of 14841 bp in length
*	132551	132750	gap of unknown length
*	132751	152071	contig of 19321 bp in length
*	152072	152317	gap of unknown length
*	152172	176190	contig of 24019 bp in length
*	176191	176290	gap of unknown length
*	176291	202324	contig of 26034 bp in length

FEATURES

```
misc_feature      1. 1576
                   /note="assembly_name:Contig4"
misc_feature      1677. 3263
                   /note="assembly_name:Contig5"
misc_feature      3364. 5443
                   /note="assembly_name:Contig6"
misc_feature      5544. 8196
                   /note="assembly_name:Contig7"
misc_feature      8297. 12038
                   /note="assembly_name:Contig8"
misc_feature      12139. 15992
                   /note="assembly_name:Contig9
                   clone.end:17
                   vector_side:right"
misc_feature      16093. 21192
                   /note="assembly_name:Contig10"
misc_feature      21293. 24766
                   /note="assembly_name:Contig11"
misc_feature      24867. 30824
                   /note="assembly_name:Contig12
                   /note="assembly_name:Contig13
misc_feature      30925. 37153
                   /note="assembly_name:Contig13"
misc_feature      37254. 45262
                   /note="assembly_name:Contig14"
misc_feature      45363. 56733
                   /note="assembly_name:Contig15
                   /note="assembly_name:Contig16
misc_feature      56834. 72156
                   /note="assembly_name:Contig16"
misc_feature      72257. 84702
                   /note="assembly_name:Contig17"
misc_feature      84803. 101052
                   /note="assembly_name:Contig18"
misc_feature      101153. 117709
                   /note="assembly_name:Contig19
                   /note="assembly_name:Contig20
                   /note="assembly_name:Contig20
```

```

clone_end:sp6
vector_side:left"
misc_feature
132751..152071
/note="assembly_name:Contig21"
misc_feature
152172..176190
/note="assembly_name:Contig22"
misc_feature
176291..202324
/note="assembly_name:Contig23"
BASE COUNT      56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

```

Query Match	20.2%;	Score 137.8;	DB 2;	Length 202324;
Best Local Similarity	92.4%;	Pred. No. 2.5e-25;		
Matches 145;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

QY	493	aaatttgaagccttaatgacacatccrattgtataatgcccacatgtgaagatggccaatga	552
Db	83500	AGTTTTTGAAGCCTTATGACACATCCATTTGATTAATGCCCAATGCTGAAGATGGCAATGAA	83441

QY	553	ataatggaagtgacagcgatcgccaacatcttggataaagaagtatgaagcctattt	612
Db	83440	ATTAATGGAAGTGAACGGGATCCCCAACATTTTGGATTAAGAAGACTATGAAAGCCTATAAT	83381

QY	613	gaagacctaaagaagaalctgttccagctata	649
Db	83380	GAAGACCTTTAAAGAAAGAGTGGTTACTCATATTTA	83344

RESULT	8
AK021919	
LOCUS	AK021919 2056 bp mRNA PRI 29-SEP-2000
DEFINITION	Homo sapiens CDNA FLJ11857 f15, clone HMBB106807, moderately similar to Homo sapiens mRNA for SP0D.

VERSION	KEYWORDS	SOURCE
AK021919.1	GI:10433216 oligo capping; fls (full insert sequence).	Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to

ORGANISM	Homosapiens	Chordata	Cranialata	Vertebrata	Euteleostomi
Eukaryota; Metazoa;					
Mammalia; Eutheria;					
Primates;					
Catarrhini; Homnidae;					
Homo.					

AUTHORS
Nishigaki, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Fujii, A., Hara, H.,
Tanase, T., Nomura, Y., Togiyasu, S., Komai, F., Hata, R., Takeuchi, K.,

Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuko, Y. and Oshima, A.
NEDO human cDNA sequencing project
Unpublished (2000)

AUTHORS Isogai, T. and Otsuki, T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao

COMMENT
Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@nri.co.jp,
TEL: 81-438-52-3951, Fax: 81-438-52-3952)
NEDO human cDNA sequencing project supported by Ministry of

sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection Helix Research Institute (supported by Japan Key Technology Center

FEATURES	University of Tokyo.
source	Location/Qualifiers
	1..2056

```
/clone="HEMBA1006807"  
/clone_lib="HEMBA1"  
/dev_stage="embryo, 10 weeks"  
/tissue_type="whole embryo, mainly head"  
/note="cloning vector: PME18SFL3"
```

Query Match	Best Local Similarity	Score	DB	Length
Matches 131: Conservative	99.2%	Pred. No. 1.1e-23;	0; Mismatches 1; Indels 0; Gaps 0;	
OY 550	gaataatggaagtgaacggatgcacacatttgataagaagtataaagccctat	609		
Db 1291	GACATAAGGAAAGCAAGCAGGATGCCAACATTTTGATAAAGAGTATGAAACCTAT	1350		
OY 610	attggaagacctaaagaagaagatcttctccacgtatcacacaaagtctctttgc	669		
Db 1331	ATTGGAAGACCTTAAGAAAGAAAGAAATCTGTCTCCACGCTATACCAACCAAGTGCTTTTATG	1410		
OY 670	cttcaactttga 681			
Db 1411	CTTCAACTTTGA 1422			
RESULT 9	AF359380	1658 bp	mRNA	PRI 12-JUL-2001
LOCUS	AF359380			
DEFINITION	Homo sapiens LANO adaptor protein (LANO) mRNA, complete cds.			
ACCESSION	AF359380			
VERSION	AF359380.1	GI:14701833		
KEYWORDS	human.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1658)			
AUTHORS	Saito, H., Santoni, M.-J., Jaulin-Bastard, F., Marchetto, S., Isnardon, D., Adelaide, J., Birnbaum, D. and Borg, J.-P.			
TITLE	LANO, a novel LAP protein directly connected to MAGUK proteins in epithelial cells			
JOURNAL	J. Biol. Chem. (2001) In press			
REFERENCE	2 (bases 1 to 1658)			
AUTHORS	Saito, H., Marchetto, S., Birnbaum, D. and Borg, J.-P.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-MAR-2001) Molecular Oncology, 0119 INSERM, 27, Boulevard del Roure, Marseille 13009, France			
FEATURES	Location/Qualifiers			
Source	1..1658			
gene	/organism="Homo sapiens"			
CDS	1..1658			
	/db_xref="taxon:9606"			
	/gene="LANO"			
	1..1575			
	/gene="LANO"			
	/note="belongs to the LAP protein family with mammalian ErbB1, Scribble and Densin-180 but contains no PDZ domain; interacts with MAGUKs (DLG) and LAP proteins (Erbin); contains LRR motifs, a LAP specific domain (LAPSD), and a C-terminal MAGUK PDZ domain binding site"			
	/codon_start=1			
	/product="LANO adaptor protein"			
	/protein_id="AAK72246.1"			
	/db_xref="GI:14701834"			
	/translation="MFHCIPLMRCNRHVESIDKRHGSIVYVEIYVARSLEELLID			

BASE COUNT	483 a	383 c	378 g	414 t
ORIGIN	NNKNEVNHADIRVTSV			
Query Match	8.9%; Score 60.8; DB 9; Length 1658;			
Best Local Similarity	47.2%; Pred. No. 2e-05;			
Matches 219; Conservative	0; Mismatches 242; Indels 3; Gaps 1;			
Qy	10	ctgagctcgcgaacaaacaaatcctcaacatctcagcagaacatcggtgtgttggaagac	69	
Db	466	CTGGAGACTGACAGAGAAATCTTCTTACATATCTTCCTGACTCTTACCCAGCTCGAAGA	525	
Qy	70	ctgaagaagacatactgtggtgttcaactatcagaagacatccctcagaattggagat	129	
Db	526	CTAGAGAACTTGATTGATTAAGAAACATGAATATATATTGGCCAGATCAATTGGAGCC	585	
Qy	130	tgtgaatactcagagagacatgattgtcttgcgaatctagaatctaattggagctgcctt	189	
Db	586	CTCTTACATCTTAAAGAAATCTCTGGTTGGATGGAATC---AACGTGAGAAATTCCTCAG	642	
Qy	190	gaattaagtaatttgaagaacagttacatttggatagatctcagcaaaagatttcagat	249	
Db	643	GAATAGGAAATCTGAGAACACTGCTGTGTTAAGTCTCTTGAACAGAGTTGGAAGA	702	
Qy	250	gtcccaatctgtgtccttgcgagatgctgaattgcagtggttgatatacagcaataac	309	
Db	703	CTTCCTGAAGAAATCAGGCGCTGACTTCATTAAAGGATTAATGATTCCTCCAGACTTA	762	
Qy	310	ctgacgcagccgcgcgaagatataagacaggtctagaagagctgcagagcttctctgtat	369	
Db	763	TTAGAAACGATTCGGAGTCCGATTCGAAACATAAAGAAACGTCAATCTTGAAAGTGAT	822	
Qy	370	aaaacaagcttgactactcctccatctccatctcagctgaaccgaaagacacacctt	429	
Db	823	CAGANTAGACTCACACAGATTGCTCGAAGCAAGTTGGGCAATGTGAAGCTCTCAGACTTA	882	
Qy	430	gtcgcagtgaggacatttggctgagagctcccaactgcaccttg	473	
Db	883	GTTCTTACGAAATTCAGCTCCTGACCCCTGCTAAAGCAATTGG	926	
RESULT 10				
LOCUS BC003193	2156 bp mRNA PRI 12-JUL-2001			
DEFINITION	Homo sapiens, similar to scribbled, clone MGC:936 IMAGE:3504090,			
ACCESSION	BC003193			
VERSION	BC003193.1 GI:13112034			
KEYWORDS	MGC.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 2156)			
JOURNAL	Strausberg, R.			
REMARK	Direct Submission			
COMMENT	Submitted (13-FEB-2001) National Institutes of Health, Mammalian			
	Gene Collection (MGC), Cancer Genomics Office, National Cancer			
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
	USA			
	NIH-MGC Project URL: http://mgc.nci.nih.gov			
	Contact: MGC help desk			
	Email: gcapbs-r@mail.nih.gov			
	Tissue Procurement: ATCC			

	D	b	148604	TAAATGATTATTCOCAGATGGGGGTGTGTGCCTTGCACTACACTGTGACTTGAATTTTAATG	148545
Oy	302		gcataacccctgacagcactgtccgcaagaatatagacaagctgaaggagtgcagagcttc	361	
D	148544	GAAATTAATATTTCAGAAATCCCTGTGCACATGTCCGTTAGTAAAGCAGCGCTTCATTTAG	148485		
Oy	362	tcttgataaaaacaagctgacctacccttc	392		
D	148484	AGTTGAATAVGAACAACCTCACCGATTATTC	148454		
	RESULT 13				
	LOCUS	AC079990/c			
	DEFINITION	AC079990	133841 bp	DNA	HTG
	ACCESSION	Norway norvegicus chromosome 4 clone RP31-327216 strain Brown			21-SEP-2000
	VERSION	AC079990	Rattus norvegicus DRAFT SEQUENCE, 5 unordered pieces.		
	KEYWORDS	AC079990.1	GI:10242411		
	SOURCE	HTG; HTGS_PHASE1; HTGS_DRAFT.			
	ORGANISM	Norway rat.			
		Rattus norvegicus			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
		Rattus.			
REFERENCE		1 (bases 1 to 133841)			
AUTHORS		Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,			
		Bouffard,G.G., Dietrich,N.L., Gupta,J., Ho,S.-L., Idol,J.,			
		Lee,Ian,S.-O., Legaspi,R., Lim,M., Maduro,O.L., Maduro,V.B.,			
		Mestrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B.,			
		Stantipop,S., Thomas,J.W., Thomas,P.J., Tlonson,E.E.,			
		Touchman,J.W., Titan,J.T., Vogt,J.L., Walker,M.A., Wetherby,K.D. and			
		Green,E.D.			
TITLE		NISC Mouse Sequencing Initiative			
JOURNAL		Unpublished			
REFERENCE		2 (bases 1 to 133841)			
AUTHORS		Green,E.D.			
TITLE		Direct Submission			
JOURNAL		Submitted (21-SEP-2000) NIH Intramural Sequencing Center, 8717			
		Grosvont Circle, Gathersburg, MD 20877, USA			
COMMENT		----- Genome Center			
		Center: NIH Intramural Sequencing Center			
		Center code: NISC			
		Web site: http://www.nisc.nih.gov			
		Contact: nisc.mouse@nhri.nih.gov			
		----- Project Information			
		Center project name: rc			
		Center clone name: 327J16			
		----- Summary Statistics			
		Sequencing vector: plasmid; n/a; 100% of reads			
		Chemistry: Dye-terminator Big Dye; 100% of reads			
		Assembly program: Phrap; version 0.990319			
		Consensus quality: 132021 bases at least Q40			
		Consensus quality: 132388 bases at least Q30			
		Consensus quality: 132461 bases at least Q20			
		Insert size: 148000; agarose-fp			
		Insert size: 197000; pulse-field-gel			
		Insert size: 133441; sum-of-contigs			
		Quality coverage: 9.91x in Q20 bases; agarose-fp			
		Quality coverage: 7.44x in Q20 bases; pulse-field-gel			
		Quality coverage: 10.99x in Q20 bases; sum-of-contigs			

*		** NOTE: This is a 'working draft' sequence. It currently			
*		* consists of 5 contigs. The true order of the pieces			
*		* is not known and their order in this sequence record is			
*		* arbitrary. Gaps between the contigs are represented as			
*		* runs of N, but the exact sizes of the gaps are unknown.			
*		* This record will be updated with the finished sequence			
*		* as soon as it is available and the accession number will			
*		* be preserved.			
*		1 8955: contig of 8955 bp in length			
*		8956 9055: gap of unknown length			
*		17867: contig of 8812 bp in length			

[illegible]

Tue Feb 26 15:53:39 2002

Pediatrics Hematology & Oncology, Texas Children's FEIGIN Center
102514, Houston, Texas 77030, USA. Telephone: 713-770-4583
margolin@bcm.tmc.edu.

FEATURES

URES	Location/Qualifiers
source	1. .1127

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CDABP0083"
/clone_lib="constructed by Y.T.M. Tsang"

```

/note=="from patient with acute lymphoblastic leukemia;
similar to Homo sapiens cDNA FLJ10470 fis, clone
NT2RP2000032 with GenBank Accession Number AK001332.1"
215 c 214 g 328 t

BASE COUNT	370 a	215 c	214 g	328 t
ORIGIN				

Query Match	8.4%;	Score 57.4;	DB 9;	Length 1127;
Best Local Similarity	47.0%;	Pred. No. 0.00015;		
Matches 178; Conservative	0;	Mismatches 201;	Indels 0;	Gaps 0;

OY	182	tgcccttgatgaagaaatttgaagcaagttacattgtagatctcaatcgaacaagt	24.1
Db	343	TACCAGTGGCAGATTTAGATTACAGAACTCAGATCTTAGATGTGAGCTACACACACA	40.22
OY	242	ttccagtgctcccaatctgctcctgsgaagtgcgaatttgacagtgttgaatcaga	30.11
Db	403	TTTCAATGATTTCCAATGAAATAGGATGTGTTGAGAACCTGACAGCATTTTGCATATCACTG	46.22
OY	302	gcataaactgaccgacctgcgcgaagatatagaacgctagagagctgcagagcttc	36.11
Db	463	GGAACAAGGGGACATTTCTGCANAAACAAATGTTTAAATCATAAAGTTGAGGACTTTGA	52.22
OY	362	tcttgataaanaacaagttgacctctccatctccatcagctcgaacctgaagaagctca	42.11
Db	523	ATCTGGACACGAACCTGCATACCTCCTCCTCCAGNAAAGTTGGTCACTCTCCAGCTCA	56.22
OY	422	ctctgttagtcgtcagtcgaggacatttgtgtgagctcccaactgcgctcttggactcat	48.11
Db	583	CTCAGCTGGAGCTGAAGGGGAAGTCGTTGGACCGCCCTGCAGGCCACACTGGGCGAAGTTC	64.22
OY	482	ccaacaccttaaaatttgtaagcctatagacaatctatlgataatgcccnaatgtgaag	54.11
Db	643	GGATGCTCAAGAAAGCGGGCTGTGTGTGGAGATCACTTTTGTGATACCTCGCACTCG	70.22
OY	542	atgcaatgnaatatgga	560
Db	703	AAGTCAAGAGGCAATTGAA	721

Search completed: February 26, 2002, 10:56:31
Job time: 19668 sec

